

SEQUENCE LISTING

SEQ ID NO: 1

Sequence Length: 40

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAAGTTGC CTGTTAGGCT GTTGGTGCTG

40

SEQ ID NO: 2

Sequence Length: 39

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGAGWCAG ACACACTCCT GYTATGGGT

39

SEQ ID NO: 3

Sequence Length: 40

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGACTGTGC TCACTCAGGT CCTGGSGTTG

40

SEQ ID NO: 4

Sequence Length: 43

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGGRCCC CTGCTCAGWT TYTTGGMWTC TTG

43

SEQ ID NO: 5

Sequence Length: 40

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGATTWC AGGTGCAGAT TWTCAGCTTC

40

SEQ ID NO: 6

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGGCKCY YTGYTSAGYT YCTGRGG

37

SEQ ID NO: 7

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGGCWTCA AGATGGAGTC ACAKWYYCWG G

41

SEQ ID NO: 8

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGTGGGGAY CTKTTTYCMM TTTTTCAATT G

41

SEQ ID NO: 9

Sequence Length: 35

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGTRTCCW CASCTCAGTT CCTTG 35  
SEQ ID NO: 10  
Sequence Length: 37  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGTATATAT GTTTGTTGTC TATTTCT 37  
SEQ ID NO: 11  
Sequence Length: 38  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGAAGCCC CAGCTCAGCT TCTCTTCC 38  
SEQ ID NO: 12  
Sequence Length: 27  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
GGATCCCGGG TGGATGGTGG GAAGATG 27  
SEQ ID NO: 13  
Sequence Length: 37  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGAAATGCA GCTGGGTCA STTCTTC 37

SEQ ID NO: 14  
Sequence Length: 36  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGGATGGA GCTRTATCAT SYTCTT 36  
SEQ ID NO: 15  
Sequence Length: 37  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGAAGWTGT GGTTAAACTG GGTTTT 37  
SEQ ID NO: 16  
Sequence Length: 35  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGRACCTTG GGYTCAGCTT GRTTT 35  
SEQ ID NO: 17  
Sequence Length: 40  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGACTCCA GGCTCAATT AGTTTCCTT 40  
SEQ ID NO: 18  
Sequence Length: 37  
Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGCTGTCTY TRGSGCTRCT CTTCTGC

37

SEQ ID NO: 19

Sequence Length: 36

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGRATGGA GCKGGRTCTT TMTCTT

36

SEQ ID NO: 20

Sequence Length: 33

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGAGAGTGC TGATTCTTT GTG

33

SEQ ID NO: 21

Sequence Length: 40

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACTAGTCGAC ATGGMTTGGG TGTGGAMCTT GCTATCCTG

40

SEQ ID NO: 22

Sequence Length: 37

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence  
ACTAGTCGAC ATGGCCAGAC TTACATTCTC ATTCCCTG 37  
SEQ ID NO: 23  
Sequence Length: 38  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGGATTTG GGCTGATTTT TTTTATTG 38  
SEQ ID NO: 24  
Sequence Length: 37  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
ACTAGTCGAC ATGATGGTGT TAAGTCTTCT GTACCTG 37  
SEQ ID NO: 25  
Sequence Length: 28  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
GGATCCCGGG CCAGTGGATA GACAGATG 28  
SEQ ID NO: 26  
Sequence Length: 382  
Sequence Type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Molecular Type: cDNA  
Original Source  
Organism: Mouse  
Immediate Source

Clone: pUC-M21-V<sub>1</sub>

Features: 1..72 sig peptide

73..382 mat peptide

Sequence

ATG GAG TCA CAT ATT CAG GTC TTT GTA TAC ATG TTG CTG TGG TTG TCT	48
Met Glu Ser His Ile Gln Val Phe Val Tyr Met Leu Leu Trp Leu Ser	
5 10 15	
GGT GTT GAT GGA GAC ATT GTG ATG ACC CAG TCT CAA AAA TTC ATG TCC	96
Gly Val Asp Gly Asp Ile Val Met Thr Gln Ser Gln Lys Phe Met Ser	
20 25 30	
ACA TCA GTA GGA GAC AGG GTC AGC GTC ACC TGC AAG GCC AGT CAG AAT	144
Thr Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn	
35 40 45	
GTG GGT ACT AAT GTA GCC TGG TAT CAA CAG AAA CCA GGG CAA TCT CCT	192
Val Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro	
50 55 60	
AAA CCA CTG ATT TAC TCG GCA TCC TAT CGG TAC AGT GGA GTC CCT GAT	240
Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Asp	
65 70 75 80	
CGC TTC ACA GGC AGT GGA TCT GGG ACA GAT TTC ACT CTC ACC ATC ACC	288
Arg Phe Thr Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Thr	
85 90 95	
AAT GTG CAG TCT GAA GAC TTG GCA GAC TAT TTC TGT CAG CAA TAT AAC	336
Asn Val Gln Ser Glu Asp Leu Ala Asp Tyr Phe Cys Gln Gln Tyr Asn	
100 105 110	
AGC TAT CCT CGG GCG TTC GGT GGA GGC ACC AAA CTG GAA ATC AAA C	382
Ser Tyr Pro Arg Ala Phe Gly Gly Thr Lys Leu Glu Ile Lys	
115 120 125	

SEQ ID NO: 27

Sequence Length: 409

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: cDNA

Original Source

Organism: Mouse

Immediate Source

Clone: pUC-M21-V<sub>II</sub>

Features: 1..57 sig peptide

58..409 mat peptide

Sequence

ATG AAA TGC AGC TGG GTC ATG TTC CTG ATG GCA GTG GTT ACA GGG 48  
Met Lys Cys Ser Trp Val Met Phe Phe Leu Met Ala Val Val Thr Gly  
5 10 15

GTC AAT TCA GAG GTT CAG CTG CAG CAG TCT GGG GCA GAG CTT GTG AAG 96  
Val Asn Ser Glu Val Gln Leu Gln Gln Ser Gly Ala Glu Leu Val Lys  
20 25 30

CCA GGG GCC TCA GTC AAG TTG TCG TGC ACA GCT TCT GGC TTC AAC ATT 144  
Pro Gly Ala Ser Val Lys Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile  
35 40 45

AAA GAC ACC TAT ATA CAC TGG GCG AAG CAG AGG CCT GAA CAG GGC CTG 192  
Lys Asp Thr Tyr Ile His Trp Ala Lys Gln Arg Pro Glu Gln Gly Leu  
50 55 60

GAG TGG ATT GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC 240  
Glu Trp Ile Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp  
65 70 75 80

CCG AAG TTC CAG GGC AAG GCC ACT ATA ACA GCA GAC ACA TCC TCC AAC 288  
Pro Lys Phe Gln Gly Lys Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn  
85 90 95

ACA GCC TAC CTG CAG CTC AGC AGC CTG ACA TCT GAG GAC ACT GCC GTC 336  
Thr Ala Tyr Leu Gln Leu Ser Ser Leu Thr Ser Glu Asp Thr Ala Val  
100 105 110

TAT TAC TGT GCT TCG GCC TAC TAT GTT AAC CAG GAC TAC TGG GGT CAA 384  
Tyr Tyr Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln  
115 120 125

GGA ACC TCA GTC ACC GTC TCC TCA G 409  
Gly Thr Ser Val Thr Val Ser Ser  
130 135  
SEQ ID NO: 28  
Sequence Length: 34  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
GATAAGCTTC CACCATGGGC TTCAAGATGG AGTC 34  
SEQ ID NO: 29  
Sequence Length: 34  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
GGCGGATCCA CTCACGTTG ATTCAGTT TGGT 34  
SEQ ID NO: 30  
Sequence Length: 43  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
GATAAGCTTC CACCATGAAA TGCACTGGG TCATGTTCTT CCT 43  
SEQ ID NO: 31  
Sequence Length: 34  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
GGCGGATCCA CTCACCTGAG GAGACGGTGA CTGA 34

SEQ ID NO: 32  
Sequence Length: 18  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
CAQACAGTGG TTCAAAGT 18  
SEQ ID NO: 33  
Sequence Length: 26  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
GAATTCCGGAT CCACTCACGT TTGATT 26  
SEQ ID NO: 34  
Sequence Length: 44  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
AGTCAGAATG TGGGTACTAA TGTAGCCTGG TACCAGCAGA AGCC 44  
SEQ ID NO: 35  
Sequence Length: 38  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
TCCTATCGGT ACAGTGGTGT GCCAAGCAGA TTCAGCGG 38  
SEQ ID NO: 36  
Sequence Length: 47  
Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GCTACCTACT ACTGCCAGCA ATATAACAGC TATCCTCGGG CGTTCGG

47

SEQ ID NO: 37

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACATTAGTAC CCACATTCTG ACTGGCCTTA CAGGTGATGG TCAC

44

SEQ ID NO: 38

Sequence Length: 47

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGCACACCAC TGTACCGATA GGATGCCGAG TAGATCAGCA GCTTTGG

47

SEQ ID NO: 39

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGATAGCTGT TATATTGCTG GCAGTAGTAG GTAGCGATGT CCTC

44

SEQ ID NO: 40

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21a-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GCA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC ACC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC CCT AGC GGT AGC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	

CTC CAG CCA GAG GAC ATC CCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
 Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
                   80                  85                  90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
 Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
           95                 100                 105

SEQ ID NO: 41

Sequence Length: 31

Sequence Type: Nucleic acid

**Strandedness:** Single

### **Topology: Linear**

Molecular Type: Synthetic DNA

## Sequence

GGTACCGACT ACACCTTCAC CATCAGCAGC C

31

SEQ ID NO: 42

Sequence Length: 31

Sequence Type: Nucleic acid

**Strandedness:** Single

### **Topology: Linear**

Molecular Type: Synthetic DNA

## Sequence

GGTGAAGGTG TAGTCGGTAC CGCTACCGCT A

31

SEQ ID NO: 43

Sequence Length: 379

Sequence Type: Nucleic acid

### **Strandedness: Double**

#### Topology: Linear

Molecular Type: Synthetic

### Original Source

**Organisms:** Mouse and human

### Immediate Source

Clone: HEF-RVL-M21b-qK

### Amino acid -19--leade

Amino acid 1 = 23:FR1

Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gin Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
-1 1 3 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gin Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GCA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45 50 55 60

TTC AGC GGT AGC GGT AGT GGT ACC GAC TAC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGG CAA GGG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 44

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GCTACCTACT TCTGCCAGCA ATATAACAG

29

SEQ ID NO: 45

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TGCTGGCAGA AGTAGGTAGC GATGTCCTC

29

SEQ ID NO: 46

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21c-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCG TTG GTA GCA ACA GCT ACA GGT

48

Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

-19

-15

-10

-5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96	
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala		
-1      1	5	10
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144	
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val		
15                  20                  25		
GGT ACT AAT GTA GCC TCG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192	
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys		
30                  35                  40		
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240	
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg		
45                  50                  55                  60		
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288	
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser		
65                  70                  75		
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	336	
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser		
80                  85                  90		
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379	
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys		
95                  100                  105		

SEQ ID NO: 47

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21d-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1  
Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT      48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19            -15            -10            -3

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC      96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
-1            1            5            10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG      144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15            20            25

GGT ACT AAT GTC GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG      192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30            35            40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA      240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45            50            55            60

TTC AGC GGT AGC GGT ACC GAC TAC ACC TTC ACC ATC AGC AGC      288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Tyr Thr Phe Thr Ile Ser Ser  
65            70            75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC      336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80            85            90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C      379  
Tyr Pro Arg Ala Phe Gly Gln Gln Thr Lys Val Glu Ile Lys  
95            100            105

SEQ ID NO: 48

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TGACAGAGTG TCCGTCACCT GTAAGGCCA

29

SEQ ID NO: 49

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TTACAGGTGA CGGACACTCT GTCACCCAC

29

SEQ ID NO: 50

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21e-gκ

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48		
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly			
-19	-15	-10	-5
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96		
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala			
-1	5	10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144		
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val			
15	20	25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192		
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys			
30	35	40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240		
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg			
45	50	55	60
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288		
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser			
65	70	75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336		
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser			
80	85	90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379		
Tyr Pro Arg Ala Phe Gly Gln Gln Gly Thr Lys Val Glu Ile Lys			
95	100	105	

SEQ ID NO: 51

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21f-gx  
Amino acid -19--1:leader  
Amino acid 1 - 23:FR1  
Amino acid 24 - 34:CDR1  
Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Gys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC ACT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105  
SEQ ID NO: 52  
Sequence Length: 26  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
GACTTCACCT TGACCATCAG CAGCCT 26  
SEQ ID NO: 53  
Sequence Length: 26  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence  
CTGCTGATGG TCAAGGTGAA GTCGGT 26  
SEQ ID NO: 54  
Sequence Length: 379  
Sequence Type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Molecular Type: Synthetic  
Original Source  
Organism: Mouse and human  
Immediate Source  
Clone: HEF-RVL-M21g-gx  
Amino acid -19--1:leader  
Amino acid 1 - 23:FR1  
Amino acid 24 - 34:CDR1  
Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT AGA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG CGG TTC GGC CAA CGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 55

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21h-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19                   -15                   -10                   -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gin Met Thr Gin Ser Pro Ser Ser Leu Ser Ala	
-1                   1                       5                       10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15                   20                       25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys	
30                   35                       40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45                   50                       55                       60	
TTC AGC GGT AGC GGT AGC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65                   70                       75	

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 56

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGACAGAGTC CAAAGCCGCT GATCTACTC

SEQ ID NO: 57

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ATCAGCGGCT TTGGACTCTG TCCTGGCTT

SEQ ID NO: 58

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21i-gx

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC ACC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
-1 1 5 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
30 35 40

CCG CTG ATC TAC TCG GCA TCC TAT CCG TAC AGT GGT GTG CCA AGC AGA 240  
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45 50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TTC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Phe Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 59

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GAGGACATCG CTGACTACTT CTGCCA

26

SEQ ID NO: 60

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AAGTAGTCAG CGATGTCCTC TGGCTG

26

SEQ ID NO: 61

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21j-gκ

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly

48

-19

-15

-10

-5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT CTG	144
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA CCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGG GGT AGC GGT ACC GAC TTC ACC TTG ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC GAC TAC TTC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAC GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	
SEQ ID NO: 62	
Sequence Length: 379	
Sequence Type: Nucleic acid	
Strandedness: Double	
Topology: Linear	
Molecular Type: Synthetic	
Original Source	
Organism: Mouse and human	
Immediate Source	
Clone: HEF-RVL-M21k-gk	
Amino acid -19--1:leader	
Amino acid 1 - 23:FR1	

Amino acid 24 - 34:CDR1  
Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT                          48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19                    -15                    -10                            -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC                          96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
-1                    1                        5                                    10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG                          144  
Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
15                    20                        25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG                          192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30                    35                        40

CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA                          240  
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45                    50                        55                                    60

TTC AGC GGT AGC GGT AGC GAC TTC ACC TTG ACC ATC AGC AGC                                  288  
Phe Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser  
65                    70                        75

CTC CAG CCA GAG GAC ATC GCG GAC TAC TTC TGC CAG CAA TAT AAC AGC                          336  
Leu Gln Pro Glu Asp Ile Ala Asp Tyr Phe Cys Gln Gln Tyr Asn Ser  
80                    85                        90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C                                  379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95                    100                        105

SEQ ID NO: 63

Sequence Length: 379

Sequence Type: Nucleic acid

### **Strandedness: Double**

### **Topology: Linear**

Molecular Type: Synthetic

### Original Source

Organism: Mouse and human

### Immediate Source

Code: HEF-BVL-M211-qk

Amino acid -19--1: leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR

Amino acid 57 - 88:FR3

**Amino acid 89 - 97:CDR3**

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-18 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
 Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
     -1      1                 5                 10

AGC GTG GGT GAC AGA GTG TCC GTC ACC TGT AAG GCC AGT CAG AAT GTG 144  
 Ser Val Gly Asp Arg Val Ser Val Thr Cys Lys Ala Ser Gln Asn Val  
     15                20                25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG 192  
 Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys  
 30 35 40

CCG CTG ATC TAC TCG GCA TCC TAT CCG TAC AGT GGT GTG CGA AGC AGA 240  
 Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
 45 50 55 60

TTC AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC  
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75

288

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

336

TAT CCT CGG GGG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

379

SEQ ID NO: 64

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CAGAGCCAAA AGTTCTTGAG CGCCAG

26

SEQ ID NO: 65

Sequence Length: 26

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CTCAGGAACT TTTGGCTCTG GGTCA

26

SEQ ID NO: 66

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21m-gx  
Amino acid -19--1:leader  
Amino acid 1 - 23:FR1  
Amino acid 24 - 34:CDR1  
Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19                    -15                    -10                    -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CAA AAG TTC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Gln Lys Phe Leu Ser Ala	
-1                    1                        5                        10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15                    20                        25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30                    35                        40	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45                    50                        55                        60	
TTC AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65                    70                        75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80                    85                        90	

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

379

SEQ ID NO: 67

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GGACAGAGTC CAAAGCTGCT GATCTACTC

29

SEQ ID NO: 68

Sequence Length: 29

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ATCAGCAGCTT TGGACTCTG TCCTGGCTT

29

SEQ ID NO: 69

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21n-gx

Amino acid 1 - 19--1:leader

Amino acid 20 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCG TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19 -15 -10 -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1 1 5 10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15 20 25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GCA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30 35 40	
CTG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Leu Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45 50 55 60	
TTC AGC GGT AGC GGT AGC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65 70 75	
CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGG CAG CAA TAT AAC AGC	336
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser	
80 85 90	
TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C	379
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys	
95 100 105	

SEQ ID NO: 70

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21c-gr

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2

Amino acid 50 - 56:CDR2

Amino acid 57 - 88:FR3

Amino acid 89 - 97:CDR3

Amino acid 98 - 107:FR4

Sequence

ATG GGA TGG AGC TGT ATC ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT	48
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly	
-19                   -15                   -10                   -5	
GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC	96
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala	
-1     1               5                   10	
AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG	144
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val	
15                   20                   25	
GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA CAG AGT CCA AAG	192
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Gln Ser Pro Lys	
30                   35                   40	
CCG CTG ATC TAC TCG GCA TCC TAT CGG TAC AGT GGT GTG CCA AGC AGA	240
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg	
45                   50                   55                   60	
TTC AGC GGT AGC GGT AGC GAC TTC ACC TTC ACC ATC AGC AGC	288
Phe Ser Gly Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser	
65                   70                   75	

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA CGG ACC AAG GTC GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 71

Sequence Length: 23

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

GCTCCAAAGC CGCTGATCTA CTC 23

SEQ ID NO: 72

Sequence Length: 23

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TAGATCAGCG GCTTTGGAGC CTT 23

SEQ ID NO: 73

Sequence Length: 379

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Original Source

Organism: Mouse and human

Immediate Source

Clone: HEF-RVL-M21p-gk

Amino acid -19--1:leader

Amino acid 1 - 23:FR1

Amino acid 24 - 34:CDR1

Amino acid 35 - 49:FR2  
Amino acid 50 - 56:CDR2  
Amino acid 57 - 88:FR3  
Amino acid 89 - 97:CDR3  
Amino acid 98 - 107:FR4

**Sequence**

ATG GGA TGG AGC TGT ATG ATC CTC TCC TTG GTA GCA ACA GCT ACA GGT 48  
Met Gly Trp Ser Cys Ile Ile Leu Ser Leu Val Ala Thr Ala Thr Gly  
-19 -15 -10 -5

GTC CAC TCC GAC ATC CAG ATG ACC CAG AGC CCA AGC AGC CTG AGC GCC 96  
Val His Ser Asp Ile Gln Met Thr Gln Ser Pro Ser Ser Leu Ser Ala  
-1 1 5 10

AGC GTG GGT GAC AGA GTG ACC ATC ACC TGT AAG GCC AGT CAG AAT GTG 144  
Ser Val Gly Asp Arg Val Thr Ile Thr Cys Lys Ala Ser Gln Asn Val  
15 20 25

GGT ACT AAT GTA GCC TGG TAC CAG CAG AAG CCA GGA AAG GCT CCA AAG 192  
Gly Thr Asn Val Ala Trp Tyr Gln Gln Lys Pro Gly Lys Ala Pro Lys  
30 35 40

CGG CTG ATC TAC TCG GCA TCG TAT CGG TAC AGT GGT GTG CCA AGC AGA 240  
Pro Leu Ile Tyr Ser Ala Ser Tyr Arg Tyr Ser Gly Val Pro Ser Arg  
45 50 55 60

TTC AGC GGT AGC GGT AGC GGT ACC GAC TTC ACC TTC ACC ATC AGC AGC 288  
Phe Ser Gly Ser Gly Thr Asp Phe Thr Phe Thr Ile Ser Ser  
65 70 75

CTC CAG CCA GAG GAC ATC GCC ACC TAC TAC TGC CAG CAA TAT AAC AGC 336  
Leu Gln Pro Glu Asp Ile Ala Thr Tyr Tyr Cys Gln Gln Tyr Asn Ser  
80 85 90

TAT CCT CGG GCG TTC GGC CAA GGG ACC AAG GTG GAA ATC AAA C 379  
Tyr Pro Arg Ala Phe Gly Gln Gly Thr Lys Val Glu Ile Lys  
95 100 105

SEQ ID NO: 74

Sequence Length: 137

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AAGAACCTG GGTCTCACT GAAGGCTCC TGCAAGGCTT CTGGCTCAA CATTAAAGAC	60
ACCTATATACT ACTGGGTGCC CCAGGCTCCA GGACAGGGCC TGGAGTGGAT GGGAAGGATT	120
GATCCTGAGG ATGGTAA	137

SEQ ID NO: 75

Sequence Length: 111

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

TGAGATCTGA GGACACAGCC TTTTATTCT GTGCAAGTGC CTACTATGTT AACCAGGACT	60
ACTGGGGCCA AGGGACCACT GTCACCGTCT CCTCAGGTGA GTGGATCCGA C	111

SEQ ID NO: 76

Sequence Length: 130

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

ACCTTCACTG AGGACCCAGG CTTCTTCACC TCAGCTCCAG ACTGCACCAAG CTGCCACCTGG	60
GAGTGAGCAC CTGGAGCTAC AGCCAGCAAG AAGAAGACCC TCCAGGTCCA GTCCATGGTC	120
GAAGCTTATC	130

SEQ ID NO: 77

Sequence Length: 132

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AAAGGCTGTG TCCTCAGATC TCAGGCTGCT GAGCTCCATG TAGGCTGTGT TCGTGGATTG	60
GTCTGCAGTG ATTGTGACTC GCCCCCTGGAA CTTCCGGTCA TATTTAGTAT TACCATCCGC	120
AGGATCAATC CT	132

SEQ ID NO: 78  
Sequence Length: 25  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence

GATAAGCTTC CACCATGGAC TGGAC

25

SEQ ID NO: 79  
Sequence Length: 25  
Sequence Type: Nucleic acid  
Strandedness: Single  
Topology: Linear  
Molecular Type: Synthetic DNA  
Sequence

GTCGGATCCA CTCACCTGAG GAGAC

25

SEQ ID NO: 80  
Sequence Length: 409  
Sequence Type: Nucleic acid  
Strandedness: Double  
Topology: Linear  
Molecular Type: Synthetic  
Original Source

Organism: Mouse and human  
Immediate Source

Clone: HEF-RVH-M21-gy1  
Amino acid -19--1:leader  
Amino acid 1 - 30:FR1  
Amino acid 31 - 35:CDR1  
Amino acid 36 - 49:FR2  
Amino acid 50 - 66:CDR2  
Amino acid 67 - 98:FR3  
Amino acid 99 - 106:CDR3  
Amino acid 107 - 117:FR4

Sequence

ATG GAC TGG ACC TGG AGG GTC TTC TTG CTG GCT GIA GCT CCA GGT Met Asp Trp Thr Trp Arg Val Phe Phe Leu Leu Ala Val Ala Pro Gly	48
-19                    -15                    -10                    -5	
 GCT CAC TCC CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG GTG AAG AAG Ala His Ser Gln Val Gln Leu Val Gln Ser Gly Ala Glu Val Lys Lys	96
-1      1                    5                    10	
 CCT GGG TCC TCA GTG AAG GTC TCC TGC AAG GCT TCT GGC TTC AAC ATT Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly Phe Asn Ile	144
15                    20                    25	
 AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA CAG GGC CTG Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly Gln Gly Leu	192
30                    35                    40	
 CAG TGG ATG GGA AGG ATT GAT CCT GCG GAT GGT AAT ACT AAA TAT GAC Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr Lys Tyr Asp	240
45                    50                    55                    60	
 CCG AAG TTC CAG GGC CGA GTG ACA ATC ACT GCA GAC GAA TCC ACG AAC Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu Ser Thr Asn	288
65                    70                    75	
 ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC ACA GCA GCC TTT Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp Thr Ala Phe	336
80                    85                    90	
 TAT TTC TGT GCA AGT GCC TAC TAT GTT AAC CAG GAC TAC TGG GGC CAA Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr Trp Gly Gln	384
95                    100                    105	
 GGG ACC ACT GTC ACC GTC TCC TCA G Gly Thr Thr Val Thr Val Ser Ser	409
110                    115	
 SEQ ID NO: 81	
Sequence Length: 84	
Sequence Type: Nucleic acid	
Strandedness: Single	
Topology: Linear	

Molecular Type: Synthetic DNA

Sequence

AGCTTGTAC CGTCTCCTCA CGTGCTCGTG GTTCGGGTGG TGCTGGTTCG GGTGGTGGCG  
GATCGGACAT CCAGATGACC CAGG

60

84

SEQ ID NO: 82

Sequence Length: 84

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

AATTGGTGGG CCATCTGGAT GTCCGATCCG CCACCAACCG AACCAACC ACCCGAACCA  
CCACCACTG AGGAGACGGT GACA

60

84

SEQ ID NO: 83

Sequence Length: 34

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CAGCCATGGC GCAGTGTGCA GCTGGTGCAG TCTG

34

SEQ ID NO: 84

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

Sequence

CCACCCGAAC CACCACCACC TGAGGGAGACG GTGACAGTGG T

41

SEQ ID NO: 85

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

**Sequence**

GGGACCACTG TCACCGTCTC CTCAGGTGGT GGTGGTTCGG G

41

SEQ ID NO: 86

Sequence Length: 41

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

**Sequence**

GGGCTCTGGG TCATCTGGAT GTCCGATCCG CCACCACCCG A

41

SEQ ID NO: 87

Sequence Length: 44

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

**Sequence**

TCGGACATCC AGATGACCCA GAGCCCAAGC AGCCTGAGCG CCAG

44

SEQ ID NO: 88

Sequence Length: 57

Sequence Type: Nucleic acid

Strandedness: Single

Topology: Linear

Molecular Type: Synthetic DNA

**Sequence**

CAAGAATTCT TATTATTTAT CGTCATCGTC TTTGTAGTCT TTGATTTCGA CCTTGGT

57

SEQ ID NO: 89

Sequence Length: 822

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

**Original Source**

Organism: Mouse and human

**Immediate Source**

Clone: pSCFVT7-hM21

Amino acid 1 - 22:leader

Amino acid 23 - 139:H chain V region

Amino acid 140 - 154:Linker

Amino acid 155 - 261:L chain V region

Amino acid 262 - 269:FLAG

Amino acid sequence of Fv polypeptide scFv-hM21 and  
nucleotide sequence coding therefor

Sequence

ATG AAA TAC CTA TTG CCT ACG GCA GCC GCT GGA TTG TTA TTA GTC GCT	5	10	15	48
Met Lys Tyr Leu Leu Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala				
GCC CAA CCA GCC ATG GCG CAG GTG CAG CTG GTG CAG TCT GGA GCT GAG	20	25	30	96
Ala Gln Pro Ala Met Ala Gln Val Gln Leu Val Gln Ser Gly Ala Glu				
GTG AAG AAG CCT GGG TCC TCA GTG AAG GTC TCC AAG GCT TCT GGC	35	40	45	144
Val Lys Lys Pro Gly Ser Ser Val Lys Val Ser Cys Lys Ala Ser Gly				
TTC AAC ATT AAA GAC ACC TAT ATA CAC TGG GTG CGC CAG GCT CCA GGA	50	55	60	192
Phe Asn Ile Lys Asp Thr Tyr Ile His Trp Val Arg Gln Ala Pro Gly				
CAG GGC CTG GAG TGG ATG GCA AGG ATT GAT CCT GCG GAT GGT AAT ACT	65	70	75	240
Gln Gly Leu Glu Trp Met Gly Arg Ile Asp Pro Ala Asp Gly Asn Thr				
AAA TAT GAC CCG AAG TTC CAG GGC CGA GTC ACA ATC ACT GCA GAC GAA	85	90	95	288
Lys Tyr Asp Pro Lys Phe Gln Gly Arg Val Thr Ile Thr Ala Asp Glu				
TCC ACG AAC ACA GCC TAC ATG GAG CTC AGC AGC CTG AGA TCT GAG GAC	100	105	110	336
Ser Thr Asn Thr Ala Tyr Met Glu Leu Ser Ser Leu Arg Ser Glu Asp				

ACA GCC TTT TAT TTC TGT GCA AGT GCC TAC TAT GTT AAC CAG GAC TAC Thr Ala Phe Tyr Phe Cys Ala Ser Ala Tyr Tyr Val Asn Gln Asp Tyr	115	120	125	384	
TGG CGC CAA GGG ACC ACT GTC ACC GTC TCC TCA GGT GGT GGT GGT TCG Trp Gly Gln Gly Thr Thr Val Thr Val Ser Ser Gly Gly Gly Ser	130	135	140	432	
GGT GGT GGT GGT TCG GGT GGC GGA TCG GAC ATC CAG ATG ACC CAG Gly Gly Gly Ser Gly Gly Ser Asp Ile Gln Met Thr Gln	145	150	155	160	480
AGC CCA AGC AGC CTG AGC GCC AGC GTG GGT GAC AGA GTG ACC ATC ACC Ser Pro Ser Ser Leu Ser Ala Ser Val Gly Asp Arg Val Thr Ile Thr	165	170	175	528	
TGT AAG GCC AGT CAG AAT GTG GGT ACT AAT GTA GCC TGG TAC CAG CAG Cys Lys Ala Ser Gln Asn Val Gly Thr Asn Val Ala Trp Tyr Gln Gln	180	185	190	576	
AAG CCA GGA AAG GCT CCA AAG CCG CTG ATC TAC TCG GCA TCC TAT CGG Lys Pro Gly Lys Ala Pro Lys Pro Leu Ile Tyr Ser Ala Ser Tyr Arg	195	200	205	624	
TAC AGT GGT GTG CCA AGC AGA TTC AGC GGT AGC GGT AGC GGT ACC GAC Tyr Ser Gly Val Pro Ser Arg Phe Ser Gly Ser Gly Thr Asp	210	215	220	672	
TTC ACC TTC ACC ATC AGC AGC CTC CAG CCA GAG GAC ATC GCT ACC TAC Phe Thr Phe Thr Ile Ser Ser Leu Gln Pro Glu Asp Ile Ala Thr Tyr	225	230	235	240	720
TAC TGC CAG CAA TAT AAC AGC TAT CCT CGG GCG TTG GGC CAA GGG ACC Tyr Cys Gln Gln Tyr Asn Ser Tyr Pro Arg Ala Phe Gly Gln Gly Thr	245	250	255	768	
AAG GTC GAA ATC AAA GAC TAC AAA GAC GAT GAC GAT AAA Lys Val Glu Ile Lys Asp Tyr Lys Asp Asp Asp Asp Lys	260	265		807	
TAATAAGAAT TCTTG				822	

SEQ ID NO: 90

Sequence Length: 45

Sequence Type: Nucleic acid

Strandedness: Double

Topology: Linear

Molecular Type: Synthetic

Features: Amino acid sequence of linker region of Fv polypeptide  
and nucleotide sequence coding therefor

Sequence

GGT GGT GGT GGT TCG GGT GGT GGT TCG GGT GGT GGC GGA TCG	45
Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser	
5 10 15	